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/organism="Mus musculus" /strain="C57BL/GJ" /db_xref="taxon:10090" /db_xref="MGD:MGI:1907315" /db_xref="MGD:MGI:1921435" /db_xref="210045H19" /sex="male" /tissue_type="tongue" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult"	prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to of sequence.[5' GAGAGARGATTCTGCAGTTAATTAAATTAATCCCCCCCCCC	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.  Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5] GARAGAGAGGATCCANGAGGTTCTTTTTTTTTTTTTTTTTTTT	Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiracka, T., Hori, F., Indian, T., Hori, F., Impotani, K., Ishi, Y., Itah, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshido, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission  JOURNAL Submission  JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome	JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  REFERENCE 4 (sites) AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.  TITLE Functional annotation of a full-length mouse cDNA collection Reference 409, 685-690 (2001)  REFERENCE 5 (bases 1 to 2738) AUTHORS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fibrida, S., Fibri	R C E E E E	JOURNAL Methods Enzymol. 303, 19-44 (1999)  REFERENCE 2 (sites)  AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  TITLE Normalization and subtraction of carterage-selected cover.

REFERENCE AUTHORS TITLE

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1758 CTAAATAACTTTGACAGAGATATGAATAGACTGGAAGAAGATGTGGTTGGCTTTCAGCT 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771 TACCAAATCACGAGCTTTTTTGCAGCTTCAAGTCGTTATGGAACTCCTGAAGAGCTGAAA 830
                                 2133 atgcaagagtttgatcaagcaattcagcatcttgaagaagcctatggtttcatgacttct 2192
                                                                                           2073 tatgataaatgccggcgtaggtttgatctaggcaattcaaagcatctgagatatcatgga 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tttcactctggaccacggggtcatcattggatgtgggactctcgccttttcaactatggg 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtttatttgatgctgttgaatgatatgattcatggtctctttcccagaggctgtcaccatt 1595
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                                                                       TACCATTATGCCAGAAGGCAGTTTAATTTAACCGACGATGACCTTCTTCGCTATAAGTTC
                                                                                                                                                                          tttccaagaggtgatctacatcttcccagtggtaaatttgttcctgggaacaattacagt 2072
                                                                                                                                                                                                               GCGTTTTGGTTGATGGACGCTGAGATGTACACGAACATGAGCGTTCTGGCCCCCTTTCACT 1550
                                                                                                                                                                                                                                                                                                                                                                                    gcattttggctgatggacaaggatatgtatgacttcatggctcttgacagaccatctact 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGATGAAGACTGGAATATGGGCAATATAGTGTATACTCTCACCAATCGACGCTACCTT 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggtgaagatgttagtggaatgccaacagtttgcattccggttgaagatggtggtgttggc 1655
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1295 ctttcactctggaccacggggtcatcattggatgtgggactctcgccttttcaactatgg 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for barley genomics
Unpublished (2000)
On Aug 21, 2000 this sequence version replaced gi:9860088
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HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development of a genetically and physically anchored EST resource
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                                                                                                                                                                                                                                                                                                                                                                                                 primer: AATTAACCCTCACTAAAGGG quality sequence stop: 679.
                                             Conservative
                                                                                                                                                                                                /clone_lib="Hordeum vulgare 5-45 DAP
HVCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                              /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0099J22f"
                                                                                                                                                         Location/Qualifiers
                                                           15.5%;
77.2%;
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                                           Score 452.4; DB 137;
Pred. No. 1.2e-115;
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae
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                                            1 (bases 1 to 801)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rami
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. au
              Development of a genetically
for barley genomics
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 CTTGAGGGAAAAATAGGGTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACTTGAG
                                                                   GGAGATGCAGATTTTCTTAGATATCGTGGAATGCAAGAGTTCGATCAGGCAATGCCCCAT
                                                                                                                                          GGCAAAGTTCTCCCTGGCAATAACAATAGTTATGATAAATGCCGCCGTAAATTTGATCTT
                                                                                                                                                            ggtaaatttgttcctgggaacaattacagttatgataaatgccggcgtaggtttgatcta
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On Jun 26, 2000 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ll: rwing@clemson.edu
primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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/tissue_pe="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
116 c 198 g 236 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0089P20f"
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Pred. No. 2.3e-112;
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 atttggacaccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaa 2047
                                                           gatcaggcttattaccatgggattaggcggagaaggatatttgaattttatgggaaatga 1987
                                                                                                                  CATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACATAAAAT 134
                                                                                                                                   catggctcttgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaat 1927
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HVcDNA0005 (Erysiphe infected & control) Hordeum vulgare
HV_CEb0022L05f, mRNA sequence.
EF065047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: AATTAACCCTCACTAAAGGG High quality sequence stop: 731.
Location/Qualifiers
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100 Jordan Hall, Clemson,
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Unpublished (2000)
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambdaZAP; Site_1:
    167 c    212 g    226 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="HY_CEb0022L05f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVcDNA0005 (Erysiphe infected & control)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="seedling green leaf"
/lab_host="SOLR"
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74.8%;
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Pred. No. 1.9e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 TGCGGTCGTGTATGCCCTTACAGAGTAAGAA 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTGGCCTTAGA 554
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                                                                                                          Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
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                       High quality sequence stop: 407
                                                               info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1770 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                         atgggaaatgaatttggacaccccgagtggattgattttccaagaggtgatctacatctt
CCTAATGGCGTAGTAGTTCCAGGGAATAACAACAGTTTTGACAAGTGCAGGCGTAGATTT 370
                                                                                                                                                  ATGGGGAATGAATTCGGCCATCCTGAGTGGATTGATTTCCCAAGGGGTGATCAACATCTT
                                                                                                                                                                                                                                                                                                                                                    ttgcacaaaatgatcaggcttattaccatgggattaggcggagaaggatatttgaatttt 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTATGACTTCATGGCTTTAGACAGACCATCCACTCCTATTATAGATCGTGGTATAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCATGACCAGGCCTTGGTTGGTGACAAGACAATTGCATTCTGGTTGATGGACAAGGAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agtcatgaccaggcccttgttggtgacaaaactattgcattttggctgatggacaaggat 1856
                                                                                                                                                                                                                                                                                                    TTGCACAAAATGATTAGGCTTATTACCATGGGCCTTGGTGGTGAAGGGTATTTAAATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=28 and 8 respectively). This library was constructed by Dr. Pa Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subsequently phosphorylated. The CDNA was then precipitated and redissolved in sterile, RNase, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' CDNA Size Fractionation column. The column eluent was then precipitated, redissolved, and ligated into Stratagene's precipitated, redissolved, and ligated into Stratagene's precipitated, redissolved, and ligated into Stratagene's precipitated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' er of the primer [GAGAGAGAGAGAGAACTAGTCTCGAG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to BcoRI adapters and subsequently should be considered and subsequently should be subseque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 100% of the white and 87.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 days (etiolated), then greenhouse grown for 5 days in potting soil. The cotyledons were flash-frozen in liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            were propagated on paper towels with distilled water for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XhoI; This cDNA library was constructed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1032-269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
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ATAGAAGGTGGCTNGAGAAGTGTGTAACTTATGCAGAAAGTCATGATCAAGCACTAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Laoo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSR7153 ITEC PSR Wheat Pericarp/Testa Library Triticum aestivum cDNA clone PSR7153, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cereals Group, John Innes Centre
Norfolk, Norwich NR4 7UH UNITED KINGDOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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Fax: 44 1603 502241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bailey P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: paul.bailey@bbsrc.ac.uk
                                                                                                                                                                   Similarity
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                                                                                                                                           Conservative
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/db_xref="taxon:4565"
/clone="PSR7153"
                                                                                                                                                                                                                                                                                       /tissue_type="pericarp/testa"
/dev_stage="3:1 mix 10:20 days post anthesis"
/note="Vector: Lambda & PII (Stratagene)"
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/cultivar="Novosibirskaya 67"
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Contact: Walbot V
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l. (bases 1 to 576)
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                              /cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
/tissue_type="embryo"
/dev_stage="14, 21, 2
                                                                                       /organism="Zea mays"
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AV442128 Arabidopsis thaliana
old Arabidopsis thaliana cDNA
AV442128
Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
/site_2: EcoRi; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
49 a 100 c 148 g 179 t
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CTTCGGAGCACCAATTCATATCACGAAA
                     cttctgagcaccaatacatatcacggaa 2215
                                                                                 GCGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGA
                                                                                                      atggaatgcaagagtttgatcaagcaattcagcatcttgaagaagcctatggtttcatga 2187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20363093
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1: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/strain-"Columbia"
/db_xref-"taxon:370"
/clone="APZ36d06_r"
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six-week old"
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/dev_stage="two to six-week old"
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                                                         GCAGATGGTACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCA
                                                                               9cagatggttcaccaccaattcccccatggttctcgagtaaagatacgcatggatactcca 809
                                                                                                                                                            aatgcagatgtcatgactcagaatgagtgtggtgtctgggagatcttttttgccgaataat 749
                                                                                                                                                                                                              gagtgggcaccaggagctacgtgggctgcattgattggagatttcaattaactggaatcct 689
                                                                                                                                                                                                                                                                                       AATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTTTTGGGAAATTTTTCTGCCTAACAAT 184
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1 (bases 1 to 639)
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Maize ESTs from various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
//dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
/site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a 0-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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Location/Qualifiers
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75.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Appels R
Div. of Plant Industry, CSI.
Canberra ACT 2601 AUSTRALIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
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                                                                                                                                                                                                                                                                                                                                                                                                       International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rudi@pi.csiro.au
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61 62 465000
                                          /note="Vector: Lambda Zap/Bluescript; Site_1: XhoI;
Site_2: EcoRI; Plants grown in Phytotron with 18C/13C
(day/night) 16 hour light. MI3 Reverse sequencing primer
                                                                                                                      /tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
                                                                                                                                                                                                                               /db_xref="taxon:4565"
/clone="CSB009H05"
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                                                                                                                                                                                                  /clone_lib="ITEC CSB Wheat Endosperm Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacat 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCACGGAAACATGAGGAAGATAAGGTGATCATCTTCGAAAGAGGAGATTTGGTATTTGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGCAATGCAGCATCTTGAGGAAAAATATGGGTTTATGACATCTGAGCACCAGTATGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcgtaggtttgatctaggcaattcaaagcatctgagatatcatggaatgcaagagtttga 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATGATGTCTACTACTTCACAACCGAACATCCGCATGACAATAGGCCACG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcg 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTACAAGGTGGCCTTAGACTCCGACGATGCACTCTNTGGTGGATTCAGCAGGCTTGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asagtacaagatagtcttggattcagatgatcctttgtttggaggctttggcaggcttag 2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCAACTTCCACTGGAGCAATAGCTTTTTTGACTACCGTGTTTGGGTGTTCCAAGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               BG551002 433 bp mRNA EST 09-APR-2001 sad31h09.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1074-1914 5' similar to TR:Q9XISS Q9XISS BRANCHING ENZYME 1
                                                                           Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                  Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                  BG551002.1
                                                                                                                                                                                                                                                                                                                                                                                                                            PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Public Soybean EST Project
                                                                Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                     (bases 1 to 433)
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Pred. No. 6.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1609 gtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgattatcgtc 1668
                                                                                                                                                                                                                                         1789 atgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttggctgatgg 1848
                                                                                                                                                                                                                                                                                                                                                                      1729 aaatgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtgtgtttctt 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1669 tocacatggotgttgotgataaatgggttgagattattcagaagagagagatgaagattgga 1728
1909 gagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggatatt 1968
                                                                                                                                                                                                                                                                                                                     123 AAATGGGTGATATTGTCCACACATTAACAAACAGAAGGTGGCTGGAAAAATGTGTAGCTT
                                                                                                                                                                                                     183 ATGCTGAAAGTCATGACCAGGCCTTGGTTGGTGACAAGACAATTGCATTTTGGTTGATGG
                                                                                        243 ACAAGGATATGTATGACTTCATGGCTTTAGACAGACCATCCACACCTATTATAGATCGTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGAATGCCAACATTCTGCCTTCCTACGCAAGATGGTGGGGTTGGCTTTGATTATCGCC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCACATGGCCATTGCAGACAAGTGGATTGAGATTCTCAAGAAGAATGATGAAGACTGGA 122
                                                                                                                                           acaaggatatgtatgacttcatggctcttgacagaccatctactcctctcatagatcgtg 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 info@genomesystems.com web site: www.genomesystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DHIOB host cells. Plant care, incculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue with Pseudomonas syringae pv. glycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mrNA pooled equally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR (hypersensitive response) by vacuum infiltrating plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="seedlings induced for HR (hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="GENOME SYSTEMS CLONE ID: Gm-c1074-1914"/clone_lib="Gm-c1074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 326; DB 155;
Pred. No. 3.1e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
1759 acaggcggtggttggaaaagtgtgtttcttatgctgaaagtcatgaccaggcccttgttg 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                      12 AAAAGAAGTGGCTTGAGAAGTGCGTCACTTATGCAGAAAGTCATGATCAAGCACTAGTTG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 GTATAGCGTTGCACAAAATGATTAGGCTTATTACCATGGGTCTTGGTGGTGAAGGGTATT 362
                                                                                                                                                                                                                                                                                       383;
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: oandersn@pw.usda.gov
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
Sequence have the named score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
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The structure and function of the expressed portion of the wheat
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Contact: Olin Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparations and DNA sequencing were performed Anderson lab (all other authors)."

91 c 121 g 138 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Wheat vernalized crown cDNA library"
/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
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/db_xref="taxon:4565"
/clone="WHE0803_A06_B11"
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                                                                                                                                                                                                                                                        855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                      Stanford University
                                                                                                                                                                                                                                                                                                                                   Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
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                                                                                                                                                                                                                           605011
                                                                                                                                                                                                                                       walbot@stanford.edu
                         /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"
                                                                       /tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                               /db_xref="taxon:4577"
/clone_lib="005 - Endosperm cDNA library from Schmidt lab"
                                                                                                                                                      /organism="Zea mays"
/cultivar="Ohio43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFZp43402123_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43402123 5', mRNA sequence.
                                       Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 734)
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                                                                                                                                                                                                                                      EST (Blum, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                 Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                        Contact: Blum H
No s1 sequence available.
This clone (DKFZp43402123) is available at the RZPD in Berlin
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                                                                                                                                                                                                   1648 gtgttggctttgattatcgtctccacatggctgttgctgataaatgggttgagattattc 1707
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                        1765 ggtggttggaaaagtgtgtttcttatgctgaaagtcatgaccag 1808
                                                                                                                  1708 agaag---agagatgaagattggaaaatgggtgacattgtacatatgctgaccaacaggc 1764
                                                                                                                                                                                                                                                                                                                              421 ATGCCTTGACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCCGATTCTA 480
                                                                                                                                                                                                                                                                                                                                                                                                             361 GAGTGGGTCAAGGTTTCTCAGGTGATTACAGTGAATATTTCGGACTACAAGTAGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AATATCGCTTTGATGGATTTCGTTTTGATGGTGTTACGTCCATGCTTTATCATCACCATG
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                                                                                                                                                                                                                                               481 TAACAATAGCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCCAGGGAG 540
    661
                                                                               601 AAGAGTTTAAAGATGAAGACTGGAACATGGGCGATATAGTATACACGCTCACAAACAGGC
                                                                                                                                                              541 GGGGTGGTTTTGACTATCGACTAGCCATGGCAATTCCAGATAAGTGGATTCAGCTACTTA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
  GCTACCTTGAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAG 704
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/db_xref="taxon:9606"
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/dev_stage="adult"
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141 c 171 g 220 t 1 others
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Pred. No. 3.1e-76;
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DEFINITION AI993785 LOCUS

AI993785 601 bp mRNA EST 08-SEP-1999 701514536 A. thaliana, Ohio State clone set Arabidopsis thaliana

08-SEP-1999

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AUTHORS
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KEYWORDS
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                                                                            JOURNAL
                      1995 caccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaaa 2048
                                                                                                                                                                                          1875 cttgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaatgatcagg 1934
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428 CATCCAGAATGGCTTGATTTTCCCAGGACCCACGCAGGCCCTCTCAGCCGCACA 481
                                                                                                                                                                                                                                                                           1815 gttggtgacaaaactattgcattittggctgatggacaaggatatgtatgacttcatggct 1874
                                                                                                                                                                                                                                                                                                                                                               1755 accaacaggcggttggttggaaaagtgtgtttttttatgctgaaagtcatgaccaggccctt 1814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1575 ttcccagaggctgtcaccattggtgaagatgttagtggaatgccaacagtttgcattccg 1634
                                                                                                                                                                  308 GTAGACAGACCATCAACTCCTCTTATCGATAGAGGAATAGCTTTGCACAAAATGATTAGG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1635 gttgaagatggtggtgttggctttgattatcgtctccacatggctgttgctgataaatgg 1694
                                                                                                                                                                                                                                                     188 ACCARTAGAAGGTGGTCAGAGAAGTGTATCTCTTATGCTGAAAGTCACGATCAAGCTCTT 247
                                                                                                                                                                                                                                                                                                                                                                                                                       128 ATAGAAATGCTCAAGAAGAGAGATGAAGACTGGCAAATGGGCGACATCATTTACACACTT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TACCCTGAAGCGATTACCGTTGGTGAAGATGTTAGTGGTATGCCAACATTCTGTATTCCT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: service@genomesystems.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: David Smoller, Ph.D.
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AI993785
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Search completed: August 10, 2001, 11:42:31 Job time: 6683 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 4 4 4 6 7 7 1 1 1 1 1 1 1	Result No.
2913 2028 1384 1381.2 1377.8 1377.8 1376.8 1371.4 1367.2 1367.2 1364	Score
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2913 3090 3074 2578 2531 3231 3231 2529 2715 2576 3033 3003	ength
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## ALIGNMENTS

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WPI; 1998-280936/23: P-PSDB; AAW62599.		Jobling SA, Safford R;		(NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.		05-NOV-1996; 96GB-0023095.		04-NOV-1997; 97WO-GB03032.		14-MAY-1998.		WO9820145-A2.		/product= SBE 11	1	212531	Key Location/Qualities		Manihot esculenta.		Starch branching enzyme; SBE; Cassava; SS.		Full length cassava tuber cDNA in pSJ107.		21-SEP-1998 (first entry)		AAV38719;		ID AAV38719 standard; cDNA; 2913 BP.	LT 1

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                      The present sequence encodes starch branching enzyme (SBE) II. I was isolated from cassava tubers. The products can be used for producing plants having altered starch quantities and qualities. They can also be used for producing altered plants such as cassa banana, potato, pea, tomato, maize, wheat, barley, oat, sweet po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Starch branching enzyme; SBE; cassava;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV38720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Full length cassava tuber cDNA in pSJ146.
                                                                                                                                                                                                                                                                                      Sequence 3090 BP;
                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                  Starch branching gene from cassava - plants giving modified starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jobling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1996;
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                                                                                                                                    caccttcactctacaaatctcagctcaccagcttccatggcggtcgaaggacctcttctg
                                                                                                                                              ---ctccactctgcaaatctcaatctaccggcttccatggctatcggaggacctcctct 117
                                                                                                                                                                                ctctccaaactctcaccgaaatggtatactacactgtatcaggcatacgttttccttgtg 170
                                                                                                                                                                                              ctctctaacttctcagcgaaatgggacactacaccatatcaggaatacgttttccttgtg 60
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atgatcagattgatggctcttcttcttcaacatatcaattagaaaccactggcacagttt
          atggtcggattgaatgctattcttcttctaacagatcaattggaagcccctggcacagttt
                                                       ctcatgaatctgactcctcaaatgtaatggtcactgcttctaaaaagagtcc---ttcctg
                                                                                                   gcctttccttcaactt---caaggaggcgttttctaggagggtcttctctggaaagtcat
                                             cttatgaatctgactcctcaaatttaactgtctctgcatctgagaaggtccttgttcctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA,
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW62600.
                                                                                                                                                                                                                                                                                                             plants.
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                                                                                                                                                                                                                                 Conservative
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Pred. No. 0;
0; Mismatches 285; Indels
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В Qy

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gtcatgatgccgagcacttcacctttgacgggtggtat	251	Db
tcatgatgcagagcacttcagctttgaagggtggtaggataaccggcctcgatccttc	238	Qy
gaaagtacaagatagtottggattcagatgatcottt 	N N	שמ
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tattcaattttcattggactagcagctattcggattaccgagttggctgcttamagccag 232	226	Qy
i tatcacggaaggatgaaagggatcaggatcattgtcttcgaggaggggaaacctcytttttg 2265 	2206 2331	Оу
atcaggcaatgcaacatcttgaagaagcctatggtttcatgacttctgagcaccagtata	227	Dр
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atctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgataaatgcc 208	20	γ <sub>0</sub>
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6 gtctccacatggctgttgctgataaatgggttgagattattcagaagagagag	166 179	Db Qy
	173	Дb
6 ttagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgattat	160	Qy
1 tgcttgtgaatgatatgattcacggtcttttccctgaggctgttaccattggtgaagatg 17	167	Дb
6 tyottyttyaatyatatyattoatyytotottoocayayyotytoaccattyytyaayaty 16	154	Qy
1 ctggcaactacaatgagtactttggatatgcaactgatgtagatgctgtgatttattt	161	ΔŒ
6 ccggcaactacaatgaatactttggatatgcaactgatgtagatgctgtggtttatttga 15	148	Qγ
1	155	Db
6 tcagatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagatttta 148	142	Qy
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tctaaggtttcttctttcaaatgcaaggtggtggttggatgagtacaagtt:gatggg	136	δδ

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                                                                                                  A cDNA clone (AAT69587) codes for potato starch branching enzyme II (BEII) (AAW19113). It was isolated from potato tuber cDNA by PCR amplification using primers (AAT69588-89) based on tryptic peptides of isolated BEII; the 5 and 3 ends of the sequence were detd. by RACE. A vector comprising the whole or a functional active part of the sequence were part 
                                                                                                                                                                                                                               Isolated potato starch branching degree of amylopectin branching potato starch
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(KHOS/)
(LARS/)
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                                          the isolated sequence (sense or antisense), plus regulatory sequences active in potato, can be used to produce transgenic potatoes. The starch obtd. from such plants will show a changed pattern of amylopectin branching and an altered amylopectin/amylose
                                                                                                                                                                                                   Claim 4; Page 12-15; 24pp; English
                                                                                                                                                                                                                                                                                                                                            Ek B,
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Sequence
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29-NOV-1995;
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LARSSON H.
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95SE-0004272
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and amylopectin/amylose
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Query Match

47.58;

Score 1384;

BB

18;

Length 3074;

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                                                                                               accacggggtcatcattggatgtgggactctcgccttttcaactatgggagctgggaggt
                                                                                                                                                               taatactttagatggactgaacatgtttgacggcacagatagttgttactttcactctgg
                                                                                                                                                                                        taatacgttggatgggctgaatatgtttgatggtacggatggtcactactttcactctgg
                                                                                                                                                                                                                                                             taaagctcatgagctaggaattgttgttctcatggacattgttcacagccatgcatcaaa
                                                                                                                                                                                                                                                                                   taaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac
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                                  2447 ggtgtacacacccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaa 2506
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                                                                                                                                                                     tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttcat 2446
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                                                                                                                                                                                                                                       matches 1677; Conserv
                                                                                                                                                                                                                                                                                                                                                     Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             Class A starch branching enzyme (SBB) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 32; Page 55-56; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9634968-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class A starch branching enzyme (psbe2con.seq - clone pSJ90).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT42631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2777 agaagaagtagcagtagtagaagaagtagtagtagaagaag 2820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amylose; viscosity; potato; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42631 standard; DNA; 2578 BP
467 agatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaag 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW06400
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                                                              410 tgataggatcagagagggggcatccctccacctggacttggtcagaagatttatgaaat 469
                                                                                          407 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                                                                                                                                    350 tggtaaactggaggagtctaaaacattaaatacttctgaagagacaattattgatgaatc 409
                                                                                                                                                                             347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
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                                                                                                                                                                                                                                              47.4%; Score 1381.2; DB 17; Length 2578; 77.3%; Pred. No. 0; 43; Indels 0; dative 0; Mismatches 493; Indels 0;
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gctggtcaacgatcttattcatgggcttttccccagatgcaattaccattggtgaagatgt
              gctgttgaatgatatgattcatggtctctttcccagaggctgtcaccattggtgaagatgt
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                                            attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg
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                                                                                                              tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttcat
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class A starch branching enzyme (SBB) has been obtained from potatoes. In class A SBE mols, a flexible N-terminal domain, Is found, which is not found in class B mols.

This sequence was obtained by direct sequencing of PCR fragments amplified from first strand cDNA. Nucleotides which could not be unambiguously assigned are indicated using standard IUPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 9; 142pp; English.
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05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1996;
703 tcggaatgaatttggtgtctgggagatttttctgccaaataatgtggatggttctcctgc
                 707 tcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggttcaccacc
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                                                                  643 ccagtcagctgccctcattggagatttcaacaattgggacgcaaatgctgacattatgac
                                                                                                                                                                                                                                                                               463
                                                                                                                                                                                                                                                                                                                                        403 tgataggatcagagagagggcatccctccacctggacttggtcagaagatttatgaaat 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                         347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
                                                                                tacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatgtcatgac
                                                                                                                                  aaaaatgggtttcactcgtagtgctacaggtatcacttaccgtgagtgggctcctggtgc
                                                                                                                                                      aaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggagc
                                                                                                                                                                                                     actgagggaggcaattgacaagtatgagggtggttttggaagctttttctcgtggttatga
                                                                                                                                                                                                                      actocgagaagaaattgacaagtatgaaggtagtotggatgcattttctcgtggctatga
                                                                                                                                                                                                                                                                       agacccccttttgacaaactatcgtcaacaccttgattacaggtattcacagtacaagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1378.4; DB 17; Length 2531; Pred. No. 0;
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                            1787 ttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttcgctgat 1846
                                                                                                                                                                                                                                                                                                1603 tagcggaatgccgacattttgtattcccgttcaagatgggggtgtttggctttgactatcg
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                                                                                                                                                                                            gctgcatatggcaattgctgataaatggattgagttgctcaagaaacgggatgsggattg
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                                                                                                                                                                   Starch branching enzyme; SBE; class
                                                                                                                                                                                            Class A starch branching enzyme (psbe2con.seq)
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Best Local Similarity
Matches 1694; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols.

The same sequence is given in Figure 8, however, nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New potato plant starch having high amylose content - also class starch branching enzyme and corresp. DNA to alter the viscosity starch; for use in food, biodegradable products, adhesives, etc.
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05-MAY-1995;
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New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of
                                                                              WPI; 1996-506170/50.
                                                                                                                     COOKE D, Debet M, Gidley MJ, Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                             (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                10-APR-1996;
05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
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      2173
                                                                                                                                                                                                                                                                                                                                                                                            1911 gtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggatatttg 1970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1551 ttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaagatgttagt 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1513
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                                                                                                                                                                                                                                                                                                                                                          1933 attgctttacacaaaatgatccgtctcattacgatgggattgggtggagaaggatacctc 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1491 aactacaatgaatactttggatatgcaactgatgtagatgctgtggtttatttgatgctg 1550
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gcaatgcaaaatctagaggagacgtatggtttcatgacttcagagcaccagtacatatcc
                                                                                                                                                                                                                                         caccttcctgatggcagagtcatcgctgggaataatggtagttatgataaatgccgacgt 2112
                                                                                                                                                                                                                                                                                                   catcttcccagtggtaaatttgttcctgggaacaattacagttatgataaatgccggcgt 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcagagagtcatgatcaagcccttgttggagacaaaacgatagctttctggctaatggat 1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gggatgccagctttttgcgttcctgtcgaagacggtggtgtgtgggttttgactaccgtcta 1692
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Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols, a flexible N-terminal domain, is found, which is not found in class B mols.

Example 1; Page 49-51; 142pp; English

New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.

WPI; 1996-506170/50.

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                                                                                                                                                                                                        Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                                                                             (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                                               10-APR-1996;
05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class A starch branching enzyme (86con.seq) cloned in QE32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42636 standard; DNA; 2576 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2511 ttggaacctgtcgccggttaagatatatcttaacaacaggttctgaagcaggaatgccat 2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2413 tccgcggagtttttcacctctgatggaaggcacgacgataggccttgctccttnatggtg 2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2271 aattttcattggactagcagctattcggattaccgagttggctgcttaaagcckggaaag 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2211 cggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctcgtttttgtattc
                                                                                                                                                                                                                                                                                                                                                    03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                         W09634968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amylose; viscosity; potato; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2653 teetttagttttegettge 2671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2571 tattgatcttcctatgttcatctgcgttgaacgaaatatattgagcctataatitgatgt 2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2473 tatgcaccgtgcagaaccgctgtagtttacgctgcagtagatgatgatgatgatgatgaa 2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2391 gatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttnatggtg 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2233 cgcaaggatgaaggagacagagtcattgtattcgagagaggtaacttgctcttcgtcttc 2292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgttcttctcttgtccccataggcctgttacccgaagatgtttaggagcaaagacagttg 2592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tacaaaatcgttttggactctgataactctttatttggaggcttcaaccggctigatgac 2412
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                                                                                                                                                                                                                            Debet M,
                                                                                                                                                                                                                                                                                           95GB-0009229
                                                                                                                                                                                                                                                                                                                   96GB-0007409
                                                                                                                                                                                                                                                                                                                                                      96WO-GB01075
                                                                                                                                                                                                                            Gidley MJ, Jobling SA, Safford
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SQ

Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;

2446	tcatgatgcagagcacttcagctttgaagggttggtacgataaccggcctcgatccttcat	2387	Qy	
2387	aaatacaaggttgccttggactcagatgatccactttttggtggcttcgggagaatt		Db	
2386	aagtacaagatagtcttggattcagatgatcctttgtttg	ũ	Ωу	
2326 2327	attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg		Qy Db	
26	cacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacc 	2207 2208	Оу	
	tcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacat		Qy Db	
2146 2147	gcaattcaaag           gagatgcagaa	2087 2088	Qy Db	
2086	acatetteceagtggtaaatttgtteetgggaacaat 	2027 2028	Qy Db	
2026	tttgaattttatgggaaatgaatttggacaccccgagtggattgatt	1967 1968	Db Qy	
	agtagcattgcacaaaatga               gatagcattgcacaagatga	و و	Qy Db	
	ggacaaggatatgtatgacttcatggctcttgacagaccatctactcctcatagatcg	1847 1848	Qy Db	
1846 1847	ttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttggctgat	1787 1788	Qy Db	
1786 1787	gaaaatgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtgtgtttc	1727 1728	Qy Db	
1726 1727	totocacatggctgttgctgataaatgggttgagattattcagaagagagag	1667 1668	Qy Db	
1666 1667	tagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgattatcg 		Qy Db	
1606 1607	gctgttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaagatgt 	1547 1548	Qy Db	
1546 1547	tactttggatatgcaactgatgtagatgctgtggtttatttgat 		Qy Db	
1486 1487	cagatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagattttac		Qy Db	
1426 1427	tctaaggtttcttctttcaaatgcaaggtggtggttggatgagtacaagtttgatgggtt	36	Qy Db	
1367		1308	Db	

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                                                                                                                                          Matches 1685;
                                                                                                                                                                                                                                                                                                         Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain
                                                                                                                                                                                                                                                 Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;
                                                                                                                                                                                                                                                                                     potatoes. In class A SBE mois., a Ilexible r is found, which is not found in class B mols.
                                                                                                                                                                                                                                                                                                                                                                             Claim 28-30; Page 42-46; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cooke D, Debet M, Gidley MJ, Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09634968-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                  starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-506170/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42630 standard; DNA; 3033 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1997 (first entry)
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  407 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                             573 tggtaaactggaggagtctaaaacattaaaatacttctgaagagacaattattgatgaatc 632
                                                                                     347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amylose; viscosity; potato; ss
                                                                                                                                                         A 46.8%;
Similarity 75.9%;
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-0007409.
95GB-0009229.
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145..288
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289..2
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145..2793
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                                                                                                                                       0;
                                                                                                                                                         Score 1364; DB 17;
Pred. No. 0;
                                                                                                                                     Mismatches 535; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New potato plant starch having high amylose content - also class starch branching enzyme and corresp. DNA to alter the viscosity starch; for use in food, biodegradable products, adhesives, etc.
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05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1996
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Westcott RJ;
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95GB-0009229.
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AAT42635
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       10-APR-1996;
05-MAY-1995;
                                                                                                                   Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                   Class A starch branching enzyme (11con.seq).
                                                                                                                                                     03-MAR-1997 (first entry)
                                                                                                                                                                                           AAT42635 standard; DNA; 2975 BP
                                  03-MAY-1996;
                                                    07-NOV-1996
                                                                                        Solanum tuberosum
                                                                                                        amylose; viscosity; potato; ss.
       96GB-0007409.
95GB-0009229.
                                  96WO-GB01075
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Best Local Similarity
Matches 1665; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New potato plant starch having high amylose content - also class starch branching enzyme and corresp. DNA to alter the viscosity estarch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                  1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class A starch branching enzyme (SBE) has been obtained potatoes. In class A SBE mols., a flexible N-terminal is found, which is not found in class B mols.
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The rice starch branching enzyme is encoded by the cDNA sequence AAQ73750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
5'UTR
                                                           Claim 1; Page 9-12; 13pp; Japanese.
                                                                                         New gene of branching enzyme of rice starch - useful for increasing starch yield of rice grains
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Matches 1592;
1377 cttctttcaaatgcaaggtggttgggttggatgagtacaagtttgatgggttcagntttgat 1436
                                                          1427 catcattggatgtgggattctcgccttttcaactatgggaattgggaagttctmagattt 1486
                                                                                        1317 catcattggatgtgggactctcgccttttcaactatgggagctgggaggttct:aggttt 1376
                                                                                                                                                                                                         1257 gatgggctgaatatgtttgatggtacggatggtcactactttcactctggaccacggggt 1316
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                                                                                                                                                                                 1367 gatgggttgaacggttttgatggtacagatacgcattactttcatagtggttc:icgcggc 1426
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aatgaatactttggatatgcaactgatgtagatgctgtgggtttatttgatgctgttgaat
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                                                                                                                                                                                                                                                                                   Query Match 44.4%;
Best Local Similarity 76.3%;
Matches 1589; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch is improved by the use of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW41763
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(MITK ) MITSUI
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                                                                                                                                                          632 gctggaaggatttcggaaccatcttgactaccgatacagtgaatacaagagaatgcgtgc
                                                                                                                                                                                                                      572 taaaccacgagttatcccaccaccaggagatgggcagaagatataccaaattgacccaat 631
                             752 attcacccgcagcgctgaaggcattacctaccgagaatgggcacctggagcacagtctgc
                                                                                                             agaaattgacaagtatgaaggtagtctggatgcattttctcgtggctatgaaaagtttgg
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                                                tttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggaagctacgtgggc
                                                                                            agctattgaccaacatgaaggtggcttggatgcattttctcgtggttacgaaaagcttgg
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                                                                                                                                                                                                                                                                                   Score 1292.6;
Pred. No. 0;
0; Mismatches
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03-APR-1998;
                                                                                                                Non-glycogen-like polysaccharide production; fermentation;
starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
non-starch branching gene; amylopectin; amylose; plant-like starch;
                          15-OCT-1998.
                                                  WO9844780-A1
                                                                             zea mays.
                                                                                                    maize branching enzyme II; ss
                                                                                                                                                                        DNA encoding maize branching enzyme II.
                                                                                                                                                                                                23-AUG-1999 (first entry)
                                                                                                                                                                                                                                                     AAV70961 standard; DNA; 2640 BP
98WO-US06660.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2640 BP;
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cgcacgttggaatgagtagtacggagccagtaattaacacatatgccaactttagagatg
                                                  agaagtatgtgttcaaaaatcctcagccaaaagagaccaaaatcacttcggatttatgagt
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                                                                     2410 ttgaagggtggtacgataaccggcctcgatccttcatggtgtacaccaccatgtagaacag 2469
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Search completed: August 10, 2001, 12:53:48 Job time: 6670 sec

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Result
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Maximum DB seq length: 2000000000
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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US-08-941-445A-14
US-09-087-277-3
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US-08-911-449-1
US-08-104-158-1
US-08-981-803-29
US-08-981-803-29
US-08-98-24-656B-1
US-08-204-656B-3
US-08-204-656B-7
US-08-204-656B-7
US-08-204-656B-7
US-08-470-702-2
US-08-470-702-2
US-08-467-831-2
US-08-467-831-2
US-08-467-831-3
US-08-261-083-7
US-08-467-831-3
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Sequence 1, Appli sequence 3, Appli sequence 16, Appli sequence 1, Appli sequence 1, Appli sequence 29, Appli sequence 3, Appli sequence 1, Appli sequence 2, Appli sequence 1, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 3, Appli sequence 3, Appli sequence 5, Appli sequence 2, Appli sequence 24, Appli sequence 
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45	44	43	42	41.	40	39	38	37	36	35	34	33	32	31	30	29	28
34	34	34	34	34	34	34	34	34.6	34.6	34.6	34.6	34.6	35	35	35	35	37
1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.3
4060	4060	4060	4060	4060	4060	4060	4060	5893	5893	1376	1376	1243	7101	7101	198	198	2100
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US-08-845-623-7	US-08-845-623-5	US-08-845-623-3	US-08-845-623-1	US-08-164-292B-7	US-08-164-292B-5	US-08-164-292B-3	US-08-164-292B-1	US-08-687-080-44	US-08-592-126-54	US-09-043-937A-7	US-08-722-184-3	US-08-687-080-53	US-08-405-496A-9	US-08-480-604A-9	PCT-US95-10668-2	PCT-US95-10668-1	US-07-927-316A-1
Sequence 7,	Sequence 5,	Sequence 3,	Sequence 1,	Sequence 7,	Sequence 5,	Sequence 3,	Sequence 1,	Sequence 44	Sequence 54	Sequence 7,	Sequence 3,	Sequence 53	Sequence 9,	Sequence 9,	Sequence 2,	Sequence 1,	Sequence 1,
Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl i	, Appl	, Appl	Appli	Appli	3, Appl	Appli	Appli	Appli	Appli	Appli

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
CONTINUES: DEFORMER: DEFOR
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SEQ ID NO 1
LENGTH: 3074
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APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: NAME/KEY: mat_peptide LOCATION: (333)..(2825)
                        NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu,
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (92)..(2156) COLORITON: (92)..(2156) COTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE: NAME/KEY: sig_peptide LOCATION: (189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Unknown Organism:bell gene OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
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ORGANISM: Unknown
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LOCATION: (189)..(2825)
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; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro
US-09-087-277-1
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LOCATION: (1404)..(1406)
OTHER_INFORMATION: Amino
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OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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OTHER INFORMATION: Amino acid 366 is Xaa wherein
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                                                                                                                                                                                              TELEFAX: (303) 499-808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY_AGENT INFORMATION:
NAME: Winner, Ellen p
REGISTRATION NUMBER: 28,547
REGISTRATION NUMBER: 28,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                           ORIGINAL SOURCE:
                                                                         TOPOLOGIE TYPE: mk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
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                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                         ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 30-SE
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    NAME/KEY:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1556;
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LOCATION:
FEATURE:
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1870 tygotottgacaagaccatotactocotocatagatogtgagtagcattgcacaaaatga 1929 | 1870 tygotottgacaagacgatocotocotocatagatogtgagtagcattgcacaaaatga 1929 | 1870 tygotottgacagatagcattgcacaagacgatagcattagcacaagaaga 1924
2345 CCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCACGCAGCCGAGCACCTTCACCG 2404
                                    2350 cagatgatcctttgtttggaggctttggcaggcttagtcatgatgcagagcacttcagct 2409
                                                                                                                                                                                                                                                                                                                                                             2230 ggatcattgtcttcgagaggggaaacctcgtttttgtattcaattttcattggactagca 2289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2170 aagcctatggtttcatgacttctgagcaccaatacatatcacggaaggatgaaagggatc 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2110 caaagcatctgagatatcatggaatgcaagagtttgatcaagcaattcagcatcttgaag 2169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1985 TTGGACATCCTGAATGGATAGATTTTCCAAGAGGTCCGCAAAGACTTCCAAGTGGTAAGT 2044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1630
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                                                                                                                                                     2285 GCTATTTTGACTACCGTATTGGTTGTCGAAAAGCCTGGGGTGTATAAGGTGGTCTTGGACT 2344
                                                                                                                                                                                                                         2290 gctattcggattaccgagttggctgcttaaagccaggaaagtacaagatagtcttggatt 2349
                                                                                                                                                                                                                                                                                                                2225 AGGTGATTGTGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAACAACA 2284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/087,2778
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                      Matches 1113;
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APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism:beII gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                FEATURE: Misc_feature NAME/KEY: Misc_feature LOCATION: (1148)..(1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (890)...(892)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa - Thr
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LOCATION: (422)...(424)
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NAME/KEY: misc_feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotide
OTHER INFORMATION: C, G or T.
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ORGANISM: Unknown
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                                                                           797 catggatactccatctggcaacaaagattctattcctgcttggatcaagttctcagttca 856
                                                                                                                                                                                y Match 32.5%; Score 947.4; DB 4; Length 1:193; Local Similarity 79.9%; Pred. No. 4.2e-281; hes 1113; Conservative 0; Mismatches 280; Indels 0;
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ggatagaccntcaacatcattaatagatcgtgggatagcattgcacaagatgattaggct
                     tgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaatgatcaggct 1936
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                                                                                                                                                                                                                                                                                         TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Keeling, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                              FEATURE:
                                                                                             LOCATION: FEATURE:
                                                                                                                                                FEATURE:
                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                           LENGTH: 2763
TYPE: nucleic
STRANDEDNESS:
                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                            NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
             LOCATION:
                               NAME/KEY:
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                                                                                                                              NAME/KEY:
                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/026,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boulder
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1208 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGGTTACATCAATGCTGTATCAT 1267
                                              1401 ttggatgagtacaagtttgatgggttcagatttgatggggtgacttcaatgatgtacacc 1460
                                                                                                          1110 tttgggtatcacgtcacaaacttttatgcagctagcagccgatttggaactcctgatgat 1169
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2135 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCA 2183
                                         2358 cctttgtttggaggctttggcaggcttagtcatgatgcagagcacttca 2406
                                                                                                    2075 GGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAGTAGCCCTGGACTC%GATGCT 2134
                                                                                                                              2298 gattaccgagttggctgcttaaagccaggaaagtacaagatagtcttggattcigatgat 2357
                                                                                                                                                                                                  2015 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACCTACGAG 2074
                                                                                                                                                                                                                                                                                                      1955 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAA(GTTATT 2014
                                                                                                                                                                                                                                                                                                                                                2178 ggtttcatgacttctgagcaccaatacatatcacggaaggatgaaagggatcggatcatt 2237
                                                                                                                                                                                                                                                                                                                                                                                                        1895 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGA(AGATTT 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                     2118 ctgagatatcatggaatgcaagagtttgatcaagcaattcagcatcttgaagaa;gcctat 2177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAACAACTGGAGCTATGATAAATGCAGACGACAGTGGAGCCTTGTGGACACTGATCAC 1894
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; Sequence 1, Application US/08716449

Patent No. 6103893

; GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
                                                                                                                                                 US-08-716-449-1
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                                                                                                                                                                                    ; IDENTIFICATION METHOD: lone ORF with homology to other iDENTIFICATION METHOD: branching enzymes ; OTHER INFORMATION: complements KV832 E. coli glycogen oTHER INFORMATION: branching enzyme mutant US-08-716-449-1
                                                                                    Query Match
Best Local Similarity
Matches 1138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00634
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
NAME: Anita E.Nador
REGISTRATION NUMBER: 1552
REFERENCE/DOCKET NUMBER: 1552
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1058-2400
TELECOMMUNICATION 1058-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: CDNA encoding st
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE: clone 1.2.1 an
ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 363-7246 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: IMB 1.44 MB High Density Diskette
COMPUTER: COMPAQ DESKPTO 590 (IBM PC compatible)
COMPUTER: COMPAQ DESKPTO 595
COMPATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                           ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: lambda Zap tuber cDNA
CLONE: 1.2.1 and E2
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                  FEATURE: open reading frame NAME/KEY: starch branching enzyme LOCATION: 44-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: BUA
CITY: Toronto
CTATE: Canada M5K 1H6
SEQUENCE CHARACTERISTICS:
LENGTH: 3128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott & Aylen
STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method for Producing Altered Starch TITLE OF INVENTION: from Potato Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                              MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: F
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: cv desiree
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                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILED CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone 1.2.1 and E2
                                                                                                      20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/716,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mature tuber
                                                                                                                                                                                                                                                        lone ORF with homology to other starch
                                                                                    0;
                                                                             Score 605.2; DB 3;
Pred. No. 1e-175;
0; Mismatches 693;
                                                                                                                      Length 3128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1556 TACCGCCTGGCAATGGCAATCCCCAGATAAGTGGATAGAATTATTTAAAGAATAAGAATGAT 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1856 GAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTGAGTGGATTGACTTCCCT 1915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1839 tggctgatggacaaggatatgtatgacttcatggctcttgacagaccatctactcctctc 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1676 TGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACAAGACCATTGCATTT 1735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1616 GAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2019 agaggtgatctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgat 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1796 GTTGATCGAGGAATTGCGCTTCACAAGATGATCCATTTTTTCACAATGGCCTTGGGAGGA 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KOSSMANN, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Francisus
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDBATE CONCENTRATION AND THE
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CEL
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2379 aggcttagtcatgatgcagagcacttca 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2259 gtttttgtattcaattttcattggactagcagctattcggattaccgagttggctgctta 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1943 AAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGATACAAGTTTATGAAT 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2243 AGAGCTGGTCATGATGTTGACCATTTCA 2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2183 TTGCCAGGGAAGTACAGAGTTGCACTGGGCAGTGATGCTTGGGAATTTGGTGGCCATGGA 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2063 CAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTTGAACGTGGTGACCTG 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003 GCATTIGATAGAGCTATGAATTCGCTCGATGAAAAGTTCTCATTCCTCGCATCAGGAAAA 2062
                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                              NUMBER OF SEQUENCES:
                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caatacatatcacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctc 2258
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                                                                                                                                                                                                                                                                                                                                 INFORMATION:
             E: Ostrolenk, Faber, Gerb & Soffen
1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                       Sonnewald,
                                                                                                                                                                                                                                                                                                         Willmitzer, Lothar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GGCAATAATTGGAGTTATGAC 1942
                                                                                                                                  AS WELL AS PLANT CELLS
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-104-158-1
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COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104.159
EILING DATE: 13-AMG-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1134; Conservative
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TELEX: 236925
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION NUMBER: DE P 41 04 782.6
APPLICATION NUMBER: DE P 41 04 782.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FATELECOMMUNICATION INFORMATION: TELEPHONE: 212-382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION: NAME: Meilman, Edward A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: I
COUNTRY:
ZIP: 10
                                                                                                                                                                                                                                                                                                                                                        540 attgacaagtatgaaggtagtctggatgcattttctcgtggctatgaaaagttiggtttc 599
780 tctcgagtaaagatacg---catggatactccatctggcaacaaagattctat:cctgct 836
                                                                                   720 ggrgtctgggagatcttttgccgaataatgcagatggttcaccaactccaattccccatggt 779
                                                                                                                                                                            660 ttgattggagatttcaataactggaatcctaatgcagatgtcatgactcagaa~gagtgt 719
                                                                                                                                                                                                                                                                  600 tcacqcagtgaaacaggaataacttatagagagtgggcaccaggagctacgtgggctgca 659
                                                                                                                                                                                                                                                                                                                      239 ATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATTTAAAAATT::GGATTC 298
                                         419 GGTGTTTGGAGTATTAGAATTCC---TGATGTTGACAGTAAGCCAGTCATTCCACACAAC 475
                                                                                                                                                                                                                              299 AACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTGCTCAGGAAGCAGAA 358
                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELUE: TUPE: Tupe: Tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: growing tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I: New York
TRY: U.S.A.
10036-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desiree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA of total tuber mRNA in pUC 19 (Hinc II)
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2...
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "for Branching enzyme I
(partial) truncated protein; 97,11 % identity to
active potato branching enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FA-1996 PCT (951-91)
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1839	779	1719 1436	1662 1376	1602 1316	1542 1256	1482 1196	1422 1136	1362 1076	1302 1016	1251 956	1191 896	1131 836	1071 776	1011 716	951 656	891 596	837 536	476
tggctgatggacaaggatatgtatgacttcatggctcttgacagaccatctactcctctc 18	tgfgtttcttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattt 18 	gaagattggaaaatgggtgacattgtacatatgctgacccaacaggcggtggttggaaaag 17 	tatogtotocacatggotgttgotgataaatgggttgagattattcagaagagagat 17 	gatgttagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgat 16 	ttgatgctgttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaa 1	tttaccggcaactacaatgaatactttggatatgcaactgatgtagatgctgtgggtttat 1	999ttcagatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagat 1 	9a99ttotaa99tttottotttoaaatgcaa9gtg9tg9ttg9atgagtacaagtttgat 1 	totggaccacggggtcatcattggatgtgggactctcgccttttcaactatgggagctgg 1	acgttggatgggctgaatatgtttgatggtacggatggtcactactttcac 1	gctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaactaat 1	ttttatgoagotagoagocgatttggaactcotgatgatttaaagtototaatagataaa 1	cagctcatggctattcaagagcattcatattatgctagtttttgggtatcacgtcacaaac 1	tatgccaactttagagatgatgtgcttcctcgcatcaaaaagctttggctacaatgctgtt 1	tcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaacaca 1	tatgatectecogaggaggagagatatgtgtteaaaaatecteagceaaagagaceaaaa 9	tggatcaagttctcagttcaagcaccaggtgaactcccatataatggcatatac 8	
868	338	.778 .495	.718 .435	661 375	601 315	541 255	481 195	135	361	.301	250 55	190 95	130	1070 775	1010 715	550	890 595	35

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APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
FEARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER APPLICATION NUMBER: 9514435.8
EARLIER APPLICATION NUMBER: 9514435.8
EARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                               QУ
                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Solanum tuberosum US-08-981-803-29
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                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 29
LENGTH: 11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08981803 Patent No. 6147279 GENERAL INFORMATION:
                                                                                                                                                                          Matches
5302 cacatgtcggcatgagcagctctgagccacgtgtaaattcgtatcgtgagtttgcagatg 5361
                                                                              5242 acaggtaccacttcaaataccctcgccctcccaaaccccgagccccacgaatctatgaag 5301
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                       970 cgcacgttggaatgagtagtacggagccagtaattaacacatatgccaactttagagatg 1029
                                                                                                   910 agaagtatgtgttcaaaaatcctcagccaaagagaccaaaatcacttcggatttatgagt 969
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                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                     Conservative
                                                                                                                                                                                         12.7%;
                                                                                                                                                                   0;
                                                                                                                                                                 Score 369; DB 3; 1
Pred. No. 8.5e-103;
0; Mismatches 315;
                                                                                                                                                                                                       Length 11478;
                                                                                                                                                                   Indels 12;
                                                                                                                                                             Gaps
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Sequence 29, Application US/08983440
Patent No. 6232122
GENERAL INFORMATION:
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                        APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674599-2003
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER APPLICATION NUMBER: 9C7-14
EARLIER FILING DATE: 1995-07-12
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(11478) OTHER INFORMATION: K stands for G or T/U
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OTHER INFORMATION: R stands for G or
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LOCATION: (1)..(11478)
OTHER INFORMATION: M Stands for A or C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation LOCATION: (1)..(114
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1501 aatactttggatatgcaactgatgtagatgctgtggtttatttgatgctgttgaatgata 1560
                                                  5782 taacttctatgctgtatgttcatcatggaatcaatatgggatttacaggaaaccataatg 5841
                                                                                1441 tgacttcaatgatgtacacccatcatggattgcaggtagattttaccggcaaccacaatg 1500
                                                                                                                                                    5722 tttccaacttgaggtggtggctagaagagtataactttgacggatttcgatttgatggaa 5781
                                                                                                                                                                                     1381 tttcaaatgcaaggttggttggttggattacaagtttgattggtttgattggtttattgiattgggt 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5482 gatatggaaacccggaggacctaaagtatctgatagataaagcacatagcttg(gtttac 5541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5422 aacattettaetatggateatttggatateatgttaeaaaettttttgetgtgagcagta 5481
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90; Conservative
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64.3%; Pred. No. 8.5e-103; Indels 12; Gaps
tive 0; Mismatches 315; Indels 12; Gaps
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US-08-528-026C-3
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                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 2426
TYPE: DNA
ORGANISM: Bacillus stearothermophilus (Strain TRBE14)
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 9900-0002.20

CURRENT APPLICATION NUMBER: US/08/528,026C

CURRENT FILING DATE: 1995-09-13

PRIOR APPLICATION NUMBER: US 08/415,152

PRIOR FILING DATE: 1995-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (385)..(392)
OTHER INFORMATION: S D sequence
NAME/KEY: misc_feature
LOCATION: (402)..(2357)
OTHER INFORMATION: P CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
1123 tcacaaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaa 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5842 agtatttcagcgaggctacagatgttgatgctgtggtctatttaatgttggccaataatc 5901
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                                                                                   1063 atgctgttcagctcatggctattcaagagcattcatattatgctagttttgggtatcacg 1122
                                                                                                                                        1003 ttaacacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctaca 1062
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                                                 cgcacattgagttgcttcctctcgtcgagcatccgctcgaccgctcgtggggctatcaag 1014
                                                                                                                   tttatacgtaccgtgagatggccgatgaactgatctcgtatgtgctcgatcatgggttta 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAKAMURA, Hiroyasu
FUJII, Kazutoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OKADA, Shigetaka
TAKATA, Hiroki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAKAHA, Takeshi
YANASE, Michiyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TERADA, Yoshinobu
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAM
                                                                                                                                                                                                      2.3%;
                                                                                                                                                                                        0;
                                                                                                                                                                                                      Score 68.4; DB 4; Pred. No. 8.3e-11;
                                                                                                                                                                                      Mismatches 231; Indels
                                                                                                                                                                                                                      Length 2426;
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                                     CLONE: p
US-08-232-463-14
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Sequence 14, Appri
5670367
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1800 Diag
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COMPUTER: IF
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                                                                                        TOPOLOGY:
                                                                                                      STRANDEDNESS:
                                                                                                                        TYPE:
                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                     nucleic acid
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                                                                                     linear
                                                                                                      single
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1252 aagtgcgcagttttcttcatcttcgaacgcattgtttttggctcgagtattaccatatcgacg
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                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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1800 Diagonal Road,
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                                                                                                                                                                                                                                    29,768
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US-08-204-656B-1
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                                        TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                               NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                             FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/204,656B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Kolchi
TITLE OF INVENTION: Variant Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Metho
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatchouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22042
1404 base pairs
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                                                                                                                                                                                                                                                US/08/204,656B
02-MAR-1994
ON: 435
                                                                                                                                                              234-252P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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US-08-204-656B-3
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REFERENCE_/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                               SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 GGATATCGTTACCAACCAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 TGCTGATGATTTGAAGTCTTTGGCACAAGAATTGCACGATCGTGATATGTTTAATGGT 350
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LOCATION: 1..1404
CTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 8110 Gatehor CITY: Falls Church
                                                                                                                                     NAME: Weiner, Marc
REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nuclei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
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                                                                                                                                                          Marc S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotides 1-1404 occasion of the Saccharomycopsis fibuligera '-amylase structural gene'
                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.30
                                                                                                                                                                                                                                                      US/08/204,656B
                                                                                                                                     32,18
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
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DESCRIPTION: /desc = "Synthetic nucleic acid"
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1160 tcctgatgatttaaaagtctctaatagataaagctcacgagttaaggtcttcttgttctcat 1219
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                                 REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Weiner, Marc S.
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 GGATATCGTTACCAACCAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 TTATGCTTATCATGGTTGGTGGATGAAGAACATATACAAAAATTAATGAAAACTTTGGTAC 290
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
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Local Similarity 56.1%;
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OTHER INFORMATION:
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LOCATION: 1..1404
                                                                                                                                                 APPLICATION NUMBER: US/08/204,656B FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
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             TELEPHONE:
                                                                       REGISTRATION NUMBER:
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGATGATTTGAAGTCTTTGGCACAAGAATTGCACGATCGTGATATGTTGAATGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1404 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                          Virginia
                                                                                                                                                                                                                                                                                                                        U.S.A.
(703) 205-8050
                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsui, Ikuo
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               (703)
                                                       Necs. 32,181
                                                                                                                                                                                                                                                                Floppy disk
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                 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Variant-Type Carbohydrate Hydrolase,
Variant Gene Of The Enzyme And Method For Producing
Oligosaccharide Using The Enzyme
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotides 1-1404
correspond to nucleotides 79-1482 in
fibuligera '-amylase structural gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid pSf'1 (Agric. Biol. Chem
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                                                     234-252P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.4; DB 1; Length 1404; Pred. No. 0.012; 0; Mismatches 61; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 1, Application US/08470702
Patent No. 5631149
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Best Local Similarity 56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                               FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1160 tcctgatgatttaaagtctctaatagataaagctcacgagttaaggtcttcttgttctcat 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
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                FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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LOCATION: 1..1404
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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    CLONE: Derived from plasmid pSf'l (Agric. Biol. Chem.
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                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Falls Church
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                                                                                                                                    APPLICATION NUMBER: US/08/470,702
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WEINER, MARC S.
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Y: U.S.A.
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HYPOTHETICAL: NO
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US-08-470-702-2
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                  APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC: S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: THM PC COMPALI)
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REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
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TYPE: nucleic acid
STRANDEDNESS: double
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(703) 205-8000
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Search completed: August 10, 2001, 12:49:44 Job time: 6506 sec

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Database :
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.Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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  1344157 seqs, 7733874588 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1382.8	1384.8	1392.4	1396.4	1467.4	1475.2	2028	2913	Score
47.5	47.5	47.8	47.9	50.4	50.6	69.6		Query Match Length DB ID
2523	2493	2542	2517	3360	3549	3090	2913	Length I
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STU011889	STSBEII	ATU22428	AB042937	AB029548	PSSBEIGEN	A92164	A92162	ID
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FEATURES
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Sequence 28 from Patent
A92162 CT.6740058
                                                                                                                                                                                          1 (bases 1 to 2913)
Safford, R. and Jobling, S.A.
SAFFORD RICHARD (GB); JOBLING STARCH CONTENT OF PLANTS
PAtent: WO 9820145-A 28 14-MAY-1998;
SAFFORD RICHARD (GB); JOBLING STEPHEN ALAN (GB)
                                                                                                                                                                                                                                                    unclassified
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                                                                                                                                                                                                                                                                                                  A92162.1 GI:6740958
                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB69496.1"
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RVFSGKSSHESDSSNWYTASKRVLPDGRIECYSSSTDOLEAPGTVSEESQVLTDVES
LIMDDRIVEDBYNKESYPMRETYSIRKIGSKPRSIPPPGRGQRIYDIDPSLTGFRQHL
LIMDDRIVEDBYNKESYPMRETYSIRKIGSKPRSIPPPGRGQRIYDIDPSLTGFRQHL
DYRYSQYKRLREEIDKYEGSLDAFSRGYEKFGFSRSETGITYREWAPGATWAALIGDE
NYRYSQYKRLREEIDKYEGSLDAFSRGYEKFGFSRSTGITYREWAPGATWAALIGDE
NYRYSQYKRLREEIDKYEGSLDAFSRGYEKFGFRSTGTITYREWAPGATWAALIGDE
NYRYSQYKRLREEIDKYEGSLDAFSRGYEKFKRYDPKRYKSLRIYESHYGMSSTEPVINTYANF
SVQAPGELPYNGIYYDPEEEKYVFKNPQPKRRKSLRIYESHYGMSSTEPVINTYANF
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                                                                                                        /note="unnamed protein product"
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E14723 Rice mRNA f
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E14724 Rice mRNA f
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U18817 Arabidopsis
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A58164 Sequence 14
AJ011885 Solanum t
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AF286317 Triticum
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ELGLLVLMDIVHSHASTNTLDGLNMFDGTDGHYFHSGPRGHHWNDSRLFNYGSWEVL
RPLLSNARWMLDEYKFDGFRFDGVTSMAYTHHGLQVDFTGNYMEYFGYYATDVDAVVYL
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DLDWKMGDIVHMLTNRRWLEKCYSYSAESHDQALVGDKTIAFWLMIKDMYDFMALDRST
PLIDRGVALHKWLTRLTPMGLGGEGYLMFMGNUFGHPFMIDFFKÜLHLDSGKEVPGNU
YSYDKCRRRFDLGNSKHLRYHGMQEFDQAIGHLEAVGFMTSBHQYLSKDERDRIV
YSYDKCRRRFDLGNSKHLRYHGMQEFDQAIGHLEAVGFMTSBHQYLSKDERDRIV
FERGNLVFVFNFHWTSSTSDYRVGLKFGKYKTVLDSDDPLFGGFGRLSHDAEHFSFE
GMYDNRRSFMVTTPCRTAVVYALVEDBVENELEPVAG" 680 g

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Query Match Best Local ( Matches 2913; 121 TTTCCTTCAACTTCAAGGAGGCGTTTTCTAGGAGGGTCTTCTCTGGAAAGTCATCTCATG 121 tttccttcaacttcaaggaggcgttttctaggagggtctttctctggaaagtcatctcatg 180 841 tcaagttctcagttcaagcaccaggtgaactcccatataatggcatatactatgatcctc 900 721 gtgtctgggagatctttttgccgaataatgcagatggttcaccaccaccaattcccxatggtt 661 TGATTGGAGATTTCAATAACTGGAATCCTAATGCAGATGTCATGACTCAGAATGAGTGTG 61 CTCCACTCTGCAAATCTACCGGCTTCCATGGCTATCGGAGGACCTCCTCTTGCC 120 61 ctccactctgcaaatctcaatctaccggcttccatggctatcggaggacctcctcttgcc 120 781 CTCGAGTAAAGATACGCATGGATACTCCATCTGGCAACAAGATTCTATTCCTGCTTGGA 781 ctcgagtaaagatacgcatggatactccatctggcaacaaagattctattcctgcttgga 721 GTGTCTGGGAGATCTTTTTGCCGAATAATGCAGATGGTTCACCACCAATTCCCCATGGTT 1 CTCTCTAACTTCTCAGCGAAATGGGACACTACACCATATCAGGAATACGTTTTC/TTGTG 60 1 ctctctaacttctcagcgaaatgggacactacaccatatcaggaatacgttttccttgtg 60 TAAATAAAGAATCTGTTCCAATGCGGGAGACAGTTAGCATCAGAAAAATTGGATCTAAAC taaataaagaatctgttccaatgcgggagacagttagcatcagaaaaattggatctaaac cccaggtgcttactgatgttgagagtctcattatggatgataagattgttgaagatgaag ttgaatgctattcttcttcaacagatcaattggaagcccctggcacagtttcagaagaat 300 CCCAGGTGCTTACTGATGTTGAGAGTCTCATTATGGATGATAAGATTGTTGAAGATGAAG Similarity Conservative 100.0%; Score 2913; 100.0%; Pred. No. 0; 0; Mismatches DB 9; 0; Indels Length 2913; 0; Gaps

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960	101 CCGAGGAGGAGAGTATGTGTTCAA	D
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531 AAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCAGAAATATATGACA 590
                             406 aaattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgaca 465
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Safford,R. and Jobling,S.A.
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PATENT: WO 9820145-A 30 14-MAY-1998;
SAFFORD RICHARD (GB); JOBLING STEPHEN ALAN (GB)
LOCATION/Qualifiers
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AESLVMEDDKNVEEDEVKKESVPLHETTSIGKSEKFRTYTENEMAPGATWAA
FRQHLDYRYSQYKRLKESIDKYEGGEDAFKFGELRYTESFHCWSSMEPIIN
LIGDENMANDRAFKLGYNAVQDIMAIGHSYYASFGRTEVTUREPAPSGRRGTEPDLKSI
IDKAHELGLLVLMDIVHSHASNNTLOGLUMFDGTDSHYFHSGSRGHHMLWDSRLFNYG
SWEVLRFLLSNARWWLEEYRFDGFREDGVTSMMYTPHGLOVAFTGNYNEYFGYATDVD
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DRFSTELDRGTALHKMIRLTHWGLGGESYLNFWGNEFGHFEWIDPFRGGRHLPWGKD
IFGNNHSYDKCRRREDLGDANYLFYHGMGEDOAMGHLEEAVGFWTSEHQYISRKDEG
DRIIVFERGNILVEVENFHWINSYSDYRVGCFKSKYKIVLDSDDGLFGGFNRLSHDAE
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                                                                                                                                                                                                             CAAGAAAGTAAAAGTAGATAAACCTAAGATCATTCCTCCACCCGGTACTGGGCAGAAAAT 722
gtacaaaagactccgagaagaaattgacaagtatgaaggtagtctggatgcattttctcg 577
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RESULT AB029548 ACCESSION KEYWORDS VERSION LOCUS 4

ORGANISM AB029548 3360 bp mRNA PLN 10-JUL-1999 Phaseolus vulgaris kbel mRNA for branching enzyme 1 complete cds. AB029548 branching enzyme 1.
Phaseolus vulgaris cDNA to mRNA.
Phaseolus vulgaris
Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta; AB029548.1 GI:5441245

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Hirokazu Matsui, Hokkaido University, Faculty of Agriculture,
Kita ku, Kita 9 Nishi 9, Sapporo, Hokkaido 060-8589, Japan
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Nozaklik. ***
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Fax:81-11-706-3635)
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                     Starch-branching enzyme cDNA from sweet potato (Ipomoea batatas) published Only in DataBase (2001) In press 2 (bases 1 to 2517) Abe, J. and Orichi, T. Direct Submission
Submitted (18-MAY-2000) Jun-ichi Abe, Kagoshima University, Faculty
                                                                                                                                                                                                                                                                                                                                           Ipomoea batatas IBE mRNA for starch branching enzyme, partial cds. aB042937
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I; Solanales; Convolvulaceae; Ipomoea
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
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of Agriculture; Korimoto 1-21-24, Kagoshima, Kagoshima 890-0065, Japan (E-mail:j_abe@chem.agri.kagoshima-u.ac.jp, Tel:81-99-285-8642)
                                                                 /TTANS181100-**PGGGQRIYEIDPLLKNFRDHLDYRFSHYRKIREAINQYEGGLE
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MODEDQAMHHLEEKYGFWAAEHGYISTGODEGDRYIFFEGYHDDRIFRSFMYYAPSRTAVVY
ATAWFFNDRAKNTUFF"
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/protein_id="BAB40334.1"
/db_xref="GI:13516907"
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/cultivar="Joy White"
/db_xref="taxon:4120"
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121 GGGTGGCTTGGAAGTATTCTCTCGTGGCTATGAGAAATTAGGTTTCACTCGGAGTGCTAC 914 gtatgtgttcaaaaatcctcagccaaagagaccaaaatcacttcgggatttatgagtcgca 973 421 ACAAGCTCCTGGTGCAATTCCTTATGATGGAATATACTATGATCCTCCAGAAG/\(\)GGAGAG 480 854 tcaagcaccaggtgaactcccatataatggcatatactatgatcctcccgaggaggagaa 913 794 acgcatdgatactccatctggcaacaaagattctattcctgcttggatcaagtictcagt 853 734 ctttttgocgaataatgocagatggttcaccaccaattccccatggttctcgagcaaagat 793 554 aggtagtotggatgcattttctcgtggctatgaaaagtttggtttctcacgcagtgaaac 613 494 acacctagattaccggtattcacagtacaaaagactccgagaagaaattgacaagtatga 553 434 tccacccggcagagggcaaagaatatatgacatagatccaagcttgacaggctttcgtca 493 61 CCATCTTGATTATAGGTTTTCGCACTATAGGAAAATCCGGGAAGCAATTAACCAGTATGA 120 1 TCCACCTGGACTTGGTCAGAGGATCTATGAGATAGACCCTCTCTTGAAAAATTTTTCGTGA 60 Match 47.9%; Local Similarity 79.7%; CTCTTTGCCAAACAATGCAGATGGCTCACCTGCAATTCCACATGGCTCTAGAG::GAAGAT 360 AGGTATCACCTATCGGGAGTGGGCTCCTGGAGCCACGTGGGCAACACTCATTGGAGATTT 240 ACGTATGGACACTCCTTCAGGCATTAAAGACTCTATTCCCGCTTGGATCAATT".CTCTGT 420 Conservative ; Score 1396.4; DB 12; Length 2517; pred. No. 0; 0; Mismatches 421; Indels 0; 0; Gaps 0

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TCACCCAGAGTGGATTGATTTCCCTAGAGGTGAACAACGCCTTCCTGATGGTTCAGTTCT
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                                                                                                     9cttattaccatgggattaggcggagaaggatatttgaatttttatgggaaatgaatttgg 1993
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                                                                                                                                                             TCTGGATAGACCAGCAACGCCAGTAATAGACCGTGGAATAGCATTGCATAAAATGATCAG
                                                                                                                                                                                   tottgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaatgatcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2054 tcctgggaacaattacagttatgataaatgccggcgtaggtttgatctaggcaattcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgatcctttgtttggaggctttggcaggcttagtcatgatgcagagcacttcagctttga
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||| || || || || | || || || ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agggtggtacgataaccggcctcgatccttcatggtgtacacaccatgtagaacagcagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGGTACCACGATGATCGTCCTCGTTCCTTCATGGTGTACGCACCCAGTAGAACTGCAGT
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                                                                                                                                                                                                                                                                                                                                                    Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, Pennsylvania State University. 103 Tyson Bldq., University Park, pA 16802. USA
                                                                                                                                                                                                                                                                                                                                                                                                      Fisher, D.K., Gao, M., Kim, K.-N., Boyer, C.D. and Guiltinan, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guilti
Two closely related cDNAs encoding starch branching
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2542)
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Arabidopsis thaliana
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U22428.1 GI:726489
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                  University, 103
/codon_start=1
/function="1,4-alpha-d-glucan:1,4-alpha-glucan
6-alpha-d-(1,4-alpha-d-glucano)-transferase"
/product="starch branching enzyme class II"
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                                                                                                          /gene="sbe2-2"
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                                                                                                                                                         /gene="sbe2-2"
<1. .2403
                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                          /strain="ecotype Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                               /tissue_type="hypocotyl"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Matches 1657; Conservative
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Best Local
                                                                 1060 acaatgctgttcagctcatggctattcaagagcattcatattatgctagttttgggtatc 1119
                                                                                                                                                                                                   1000 taattaacacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggct 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520 acaaaagactccgagaagaaattgacaagtatgacagtctggatgcattttctcgtg 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 ATGAGATAGACCCCATGTTACGAACTTACAACAATCATCTTGATTACCGTTATGGACAGT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 atgacatagatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagt 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 TCAAGGAGAGAGGGGTGAAACCAAGAATAGTTCCCCCACCGGGTGATGGCAAGAAAATTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 tonganaanttggatotanaccanggtocattootocaccoggongagggonanagantat 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 caggagctacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatg 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 gctatgaaaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcac 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ATAAAAGATTGCGTGAGGAAATAGACAAGTATGAGGGTGGTCTTGAGGCATTCTCTCGTG 481
962 ATAATGCTGTTCAAATTATGGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACC 1021
                                                                                                                                                        902 TGGTCAATACGTATGCTAACTTTAGAGATGATGTTCTTCCCCCGCATCAAAAAGCTTTGGAT 961
                                                                                                                                                                                                                                                                                                       842 AGAGACCTAAGTCGCTAAGGATTTATGAAGCACATGTTGGCATGAGTAGCACGGAACCAA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                              662 CGCCTGCAATTCCTCATGGCTCACGTGTAAAGATTCGTATGGATACTCCATCTGGCATTA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             760 caccaccaattccccatggttctcgagtaaagatacgcatggatactccatctggcaaca 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602 TCATGACTCGGAATGAATTTGGTGTTTGGGAGATCTTTTTGCCCAACACACTGATGGTT 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 GCTATGAAAAGTTAGGATTTTCGCGCAGTGATGCCGGTATAACTTATAGAGAGTGGGCGC 541
                                                                                                                                                                                                                                                                                                                                                            agagaccaaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccag 999
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FCIFYQDGGVGEDYRLHMAIADKMIEMLKKRDEDWOMGDIIYTLINRWSEKCISYAE
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KPGKYKIVLDSDDPLFGGFNRLDRKAEYFTYDGLYDERPCSFMYVAPCRTAVVYALAN
KFG
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                                                                                                                                                                                                                                                                                                                                                                                                                    1622 AAGACTGGCAAATGGGCGACATCATTTACACACTTACCAACAGAAGGTGGTCAGAGAAGT 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1562 ACTACCGTTTACACATGGCCATAGCTGATAAGTGGATAGAATGCTCAAGAAGAGAGATG 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1660 attatogtotocacatggotgttgctgataaatgggttgagattattcagaagagagatg 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1502 AAGATGTTAGTGGTATGCCAACATTCTGTATTCCTGTCCAAGATGGTGGCGTTGGATTTG
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                                                                                                                                                                                                                                                                                                                                                          1900 tagatcgtggagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggag 1959
                                                                                                                                                                                                                                                                                                                                                                                          1840
2200 aatacatatcacggaaggatgaaagggatcagaatcattgtcttcgagagggganacctcg
                                         2042 AATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGACTTCGGAGCACC 2101
                                                                                                                                                                      2020 gaggtgatctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgata 2079
                                                                                                                                                                                                                                    1802 TCGATAGAGGAATAGCTTTGCACAAAATGATTAGGCTTATAACTATGGGATTACGCGGTG 1861
                                                                        2140 agtttgatcaagcaattcagcatcttgaagaagcctatggtttcatgacttct;agcacc 2199
                                                                                                          1982 AATGCCGCCGCAGATTTGATCTTGGGGATGCAGATTATCTCAGATACCGCGGACTACAAG 2041
                                                                                                                                    2080 aatgeeggegtaggtttgatetaggeaatteaaageatetgagatateatggaattgeaag 2139
                                                                                                                                                                                                                                                                                                                                                                                   ggctgatggacaaggatatgtatgacttcatggctcttgacagaccatctactcctctca 1899
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RESULT
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ORGANISM
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TITLE
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Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
Magnoliophyta; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 2493)
Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H.
Molecular cloning and characterization of starch-branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-JUN-1997) Larsson C.T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSBEII 2493 bp
Solanum tuberosum mRNA
AJ000004
AJ000004.1 GI:2764395
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Larsson, C.T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sbe-II gene; starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research,
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                                YDPPEEERY IFQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYN
AVQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSH
                                                                                                        /db_xref="01:2764396"
//db_xref="$PTREMS1:049953"
//db_xref="$PTREMS1:049953"
//translation="reks1:049953"
//translation="reks1:0499
{	t ASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEF}
                                                                                                                                                                                                                                                                                                                                                                                 /product="starch branching enzyme II, SBE-II"
/protein_id="CAA03846.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /plasmid="pALSBE-II (#123)"
/cultivar="Amanda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic Center, Swedish University of Agricultural Box 7055, S-750 07 Uppsala, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number="2.4.1.18"
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KFDGFREDGYTSIMYTHHGLSVGFTGNYKEYFGLATDVDAVVYLMLVNDLIHGLFPDA
ITIGEDYSGMPTFCIPVQDGGYGFDYRLHMAIADKWIELLKKBEDWRYGDIVHTLTN
RRWSEKCVSYAESHDQALVGDKTIAFWLMDKDWYDFMALDRPSTSLIDRGIALHKNI
LVTMGLGGGGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGIR
AEYLRYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNUFVENFHW
TKSYSDYRIGCLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYA
                                                                                                                                                         PSRTAVVYALVDKEEEEEEEVAVVEEVVVEEE *
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Score 1384.8;
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taaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac
                                                                      aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga 1186
                                                    GGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCAC
                                                                                                                                                                                                         cacatatyccaactttagagatyatytycttcctcycatcaaaaagcttygctacaatyc 1066
                                                                                                                                                                                                                                                                                                                                          atactatgatcctcccgaggaggagaagtatgtgttcaaaaatcctcagccaaagagacc
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                                       2267 attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg 2326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1367
2205 CTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGG 2264
                                                                                                                                     2145 ATCACGAAAGGATGAAGGAGATAGGATGTTTGTATTTGAAAAAAGGAAACCTAGTTTTTGT 2204
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                                                                                                                                                                                                                                                                       2085 CCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                         2025 ACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGA 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1965 ACAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2027 tctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgataaatgccg 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1905 CCTAAATTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTCATTTCCCTAGGGCTGA 1964
                                                                                                                                                                     atcacggaaggatgaaagggatcggatcattgtcttcgagagggggaaacctcgtttttgt 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcgtaggtttgatctaggcaattcaaagcatctgagatatcatggaatgcaagagtttga 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagattttac 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taatacgttggatgggctgaatatgtttgatggtacggatggtcactactttcactctgg 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCATCAACATCATTAATAGATCG 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttggctgat 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTC 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tctccacatggctgttgctgataaatgggttgagattattcagaagagagatgaagattg 1726
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                                                                                                                                                                                                                                                                                                               tcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacat 2206
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Jobling, S. A., Schwall, G.P., Westcott, R.J., Sidebottcm, C.M., Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum tuberosum I.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SFE II Unpublished
2 (bases 1 to 2523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2523)
Jobling, S.A.
Direct Submission
Submitted (07-CCT-1998) Jobling S.A., Plant Science
Research, Colworth House, Sharnbrook, Bedford, MK44
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/Codon_start=1
//Codon_start=1
//protedi_id="starch branching enzyme II"
//protedi_id="starch branching enzyme II"
//protedi_id="CAB40747 l"
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//db_xref="GI:4584511"
//db_xref="GI:4584511"
//translation="ILAEKSSYNSEFRESTVAASGKVLVPGT(;SDSSSSSTNOFEFTE
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TSPENSPASTPVNSSTWEHASQIKTENDDVEPSSDLTGSVEEI.DFNSVQYKKLR
EAIDKYEGGIEAFSRGYEKMGETRSATGITYREWAPGAOSAAI.TGPENWEDANDIMT
RNEFGGWEIFLENNVDGSPAIPGGSVKIRMDTPSGVKDSIP;WINYSLQLPDEIPYN
GIYYDPPEEBRYIFQHERPKKERSLRIYESHIGMSSPEERIN;WYNFEDEVLPRIKL
GYNALOIMAIDEHSY'ASFGYUYTNFFAAPSSRFGTPDDLKSL;DSAHELGIVVLMDIV
HSHASNNTLDGLNMFDGTDSCYFHSGARGYHWMMDSRLFNYGHWEVLRVLLSNARWHL
DEFKFDGFFFDGVTSMMYTHHGLSVGFFGNYEEFFFGLATDVD/NVYLMLNVNDLHGLF
PDAITIGEDVSGMFTFCIPVODGGVGFDYRLHWAIADKWIELLKKRDEDWRVGDIVHT
LTNRRWSEKCVSYAESHDOALVGDKTIAFWLNDKDMYDEMALDRESTSLLDRGIALHK
MIRLYTMGLGGEGYLNFMGNEFGHPEWIDFPRAEOHLSDDSV::PGNQFSYDKCRRRFED
LGDAEYLRYGGGGEGYLNFMGNEFGHPEWIDFPRAEOHLSDDSV::PGNQFSYDKCRRRFED
LGDAEYLRYGGGGEGFGRYKVALDSNDEPFRAEOHLSDDSV::FTFEGWYDDRPRSIM
FHWTKSYSDYRIGCLKFGKYKVALDSNDEPFRAEOHLNAE:FTFEGWYDDRPRSIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; starch branching enzyme II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="sequence SBE A-5" <2. .10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
/cultivar="Desiree"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SBE II"
<2. .2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="1,4-alpha-Glucan branching enzyme"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SBE II"
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Bedford, MK44 1LQ,
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taaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac
                                                                                                                               tgttcagctcatggctattcaagagcattcatattatgctagtttttgggtatcacgtcac 1126
                                               aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga
                                                                                                              GCTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCAC
                                                                                                                                                                                            cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc
                                                                                                                                                                           CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC
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/EC_number="2.4.1.18"
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CTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGG
                                                                                            atcacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctcgtttttgt 2266
                                                                      ATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAAGGAAACCTAGTTTTTGT
                                                                                                                                              CCGGGCTATGCAGTATCTTGAAGATAATATGAGTTTATGACTTCAGAACACCAGTTCAT
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                                                                                                                                                                                                                                                                                        ACAACACCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAG
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707 tcagaatgagtgtggtgtcttgggagatcttttttgccgaataatgcagatggttcaccacc 766
                                                          650 CCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGAC 709
                                                                                   647 tacgtgggctgcattgattgggagatttcaataactggaatcctaatgcagatgtcatgac 706
                                                                                                                                                         587 aaagtttggtttctcacgcagtgaaacaggaattaacttatagagagtgggcaccaggagc 646
                                                                                                                                                                                                                                                                                            470 AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAA 529
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                                                                                                                                       590 AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGC 649
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Cooke, D., Debet, M., Gidley, M.J., Jobling, S.A., Safford, F. Sidebottom, Christopher, M. and Westcott, R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION Patent: WO 9634968 A 19 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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COOKE, D. Debet, M., Gidley, M.J., Jobling, S.A., Sidebottom, Christopher, M. and Westcott, R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPACTED BY THE CHEM INVEST (US)
Other publication AU 5509996 961121.
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             accacggggtcatcattggatgtgggactctcgccttttcaactatgggagcttgggaggt
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                                                                                                                                                                                                                                   GGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCAC
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AGCTCGTGGTTATCATTGGATGTGGGATTCCCCGCCTCTTTAACTATGGAAACTGGGAGGT
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2383 TCATAATGCCGAATATTTCACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTAT 2442
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1787 ttatgctgaaagtcatgaccaggcccttgtttggtgacaaactattgcattttggctgat 1846
1783 aTMCGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGAT 1842
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                                                                                                      2323 AAAATACAAGGTTGGCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGA 2382
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COOKE, D., Debet, M., Gidley, M.J., Jobling, S.A., Safford, R., Sidebottom, Christopher, M. and Westcott, R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION PAtent: WO 9634968 A 18 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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COOKe,D., Debet,M., Gidley,M.J., Jobling,S.A.,
Sidebottom, Christopher,M. and Westcott,R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COM
Patent: WO 9634968-A 16 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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1066	07 cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc	Db Qy
1006	47 aaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaa 	Db Oy
946 947	atactatgatcctcccgaggaggagaagtatgtgttcaaaaatcctcagccaaagagacc 	Оy
886 887	27 tattcctgcttggatcaagttctcagttcaagcaccaggtgaactcccatataatggcat	ОУ
826 829	7 aatteeeeatggttetegagtaaagataegeatggataeteeatetggeaacaaagatte	ОУ
766 769	07 tcagaatgagtgtgtgtctgggagatctttttgccgaataatgcagatggttcaccacc 	Оγ
706 709	47 tacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatgtcatgac 	ОУ
646 649	87 aaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggagc 	Оy
586 589	7 actccgagaagaaattgacaagtatgaaggtagtctggatgcattttctcgtggctatga 	Qу
526 529	67 agatecaagettgaeaggetttegteaacacetagattaeeggtatteaeagtaeaaaag 	Qу
466 469	7 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 	Оу
406 409	jatgaagtaaataagaatctgttccaatgcgggagacagttagcatcagaaa 	Qу Дъ

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BASE COUNT
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TITLE
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                        mat_peptide
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Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure
cloning and characterisation of multiple forms of SBE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jobling, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SBEII gene; starch branching enzyme II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STU011888 2982 bp mRNA for starch branching enzyme II, sequence SBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                             888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Translation="WYTTLGGVRFPTVPSVYKSNGFSSNGDRRNANISVFLKKHSLSR
KILAEKSSYMSESRPSTLAASGKVLYPGIQSDSSSSSTDQFBRANISVFLKKHSLSR
KILAEKSSYMSESRPSTLAASGKVLYPGIQSDSSSSSTDQFBRANISVFLKKHSLSR
KILAEKSSYMSESRPSTLAASGKVLYPGIQSDSSSSSTDQFBRANISPSPRNSPSSDLTGSVEELDAASSLQLQDGGKLEESKTLNTSEFT11
STYMEHARQIKTENDDVBPSSDLTGSVEELDAASSLQLDFNTSREFGYWEIFLLNTSEFT11
DESDRIRERGIPPGIGQKIYEIDPLLTMYRQHLDYRYSQYKKLEBAIDKYEGGLEAF
SRGYERMGFFTRSAFGITYREWAPGAQSAALIGDFNNNDANDANDSMTENBEFGYWEIFLLN
NUOGSPALPHGSKYKIRNDTPSGVKDSIPAMAINYSLAPDEFNIKTLGTNAVQUMAJOEH
SYNASFGYHTNEFSHIGMSSPEPKINSYVMFRDEFLPRIKTLGTNAVQUMAJOEH
SYNASFGYHTNFFAPSSRFGTPDDLKSLIDKAHELGIVLAMIVHTLTNERHASNNTLDGLN
MFDGTDGCYFHGGARGYHMMNDEBKLENGMEPLRYLLSNARWMLDEFKFDGFRFDGV
TSMMCTHHGLSVGFTGNYEEYFGLATDVDAVVLMLTVNDLIHGLFPDAITIGEDVSGN
PTFCVPVQDGGVGFDYRLHMAIADKWIELLKKRDDEWRYGDIVHTITNRRMSEKCYSY
AFGCHOAN TVOTFORT AFGUT HOTWANDENATIONSTORM
                                                                                                                                                                                                                                                                                                                                                                                 AESHDOALVGDKTIAFWIMDKDMYDFMAIDRESTSLIDRGIALHKMIRLVTMGLGGEG
YLNEWGNEFGHPEWIDFPRAEQHLSDGSVIPRNQFSYDKCRRREDLGDAEYLRYRGLQ
EFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHMTKGYSDYRIG
                                                                                                                               /product="starch branching enzyme II" 529 c 703 g 862 t
                                                                                                                                                                                                                                                        /gene="SBE II"
284. .2773
                                                                                                                                                                                                                                                                                                                                       CLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYAPSRTAVVYAL
VDKEEEEEEEVAVVEEEVVVEEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="sequence SBE 140. .283
                                                                                                                                                                                       /gene="SBE II"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="starch branching enzyme II"
/protein_id="CAB40746.1"
/db_xref="GI:4584509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name="1,4-alpha-Glucan branching
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SBE II"
140. .2776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Solanum tuberosum"
/cultivar="Desiree"
/db_xref="taxon:4113"
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  47.0%;
76.4%;
  Score 1370.4;
Pred. No. 0;
No.
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                       Length 2982;
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                1367 totaaaggtttottotttoaaatgcaaggtggttggttggatgagtacaagtttgatgggtt 1426
                                                                                                                                                                                                                                                                                                                                                                                                1288 GGTGCAAATTATGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      628 TGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
                                                                                                  accaoggggtcatcattggatgtgggactctcgccttttcaactatgggaggttggggaggt 1366
                                                                                                                                                                                                                                     TAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAA 1467
                                                                                                                                                                                                                                                                                                                  aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga 1186
ACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATT 1647
                                                                         AGCTCGTGGTTATCATTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAACTGGGAGGT 1587
                                                                                                                                                       TAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGG
                                                                                                                                                                                taatacgttggatgggctgaatatgtttgatggtacggatggtcactactttcactctgg 1306
                                                                                                                                                                                                                                                          taaageteaegagttaggtettettgtteteatggatattgtteatageeatgcateaae 1246
                                                                                                                                                                                                                                                                                                                                                                                                                     tgttcagctcattggctattcaagagcattcatattatgctagtttttgggtatcacgtcac 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGTCGGTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaa 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGTCAGCTGCCCTCATTGGGGATTTCAACAATTGGGACGCAAATGCTGACTTTATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atactatgatcctcccgaggaggagaagtatgtgttcaaaaatcctcagccaaagagacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcagaatgagtgtgtctgggagatctttttgccgaataatgcagatggttcaccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1787 ttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcatttttggctgat 1846
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2668
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                                                  2447 ggtgtacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaa 2506
                                                                                                                   2608 TCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTAT 2667
                                                                                                                                                                                                                                   2548 AAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGA 2607
                                                                                                                                                                                                                                                                     2327 aaagtacaagatagtcttggattcagatgatcctttgttttggaggctttggcaggcttag 2386
                                                                                                                                                                                                                                                                                                                                                                                         2267 attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg 2326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2368 CCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT 2427
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                                                                                                                                                                      2387 tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttcat 2446
                                                                                                                                                                                                                                                                                                                                                   2488 CTTTAATTTTCACTGGACAAAAGGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGG 2547
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   GGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGA 2727
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core &udicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core &udicots;
Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-DEC-1994) Dane K. Fisher, Department of Horticulture, The Pennsylvania State University, Biotechnology Institute, 103 Tyson Building, University Park, PA 16802, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2668). Kim, K.N., Boyer, C.D. and Guiltinan, M.J. Fisher, D.K., Gao, M., Kim, K.N., Boyer, C.D. and Guiltinan, M.J. Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana.
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/ function="1,4-alpha-d-glucan:1,4-alpha-glican
/ function="1,4-alpha-d-glucan:1,4-alpha-glican
6-alpha-d-(1,4-alpha-d-glucano)-transferase
/ protein="starch branching enzyme class II"
/ protein_id="starch branching enzyme class II"
/ protein_id="starching enzyme c
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/db_xref="taxon:3702"
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/dev_stage="3 day-old seedling"
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/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                    DDSAEFFTSDGRHDDRPCSFMVYAPCRTAVVYAAVDDDDDDERSSLVPIGLLPEDV"
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    Score 1366.6; DB 14; Length 2668; Pred. No. 0;
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PRECTICGGAAGCCATCGTATGATTCTGATTGAT	1191 gctcacgagttagg	131 ttttatgcagctag	071 cagctcatggctat               081 CAGATAATGGCCAT	.011 tatgccaactttag	951 tcacttcggattta                   961 TCGCTGCGTATATA	891 tatgatcctcccgag                 901 TATGACCCTCCTGAG	1 cctgcttggatcaa               1 ccagcrrggarcaa	771 ccccatggttctcg 	711 aatgagtgtggtgt                   721 AACGACTTTGGTGT	651 tgggctgcattgat            661 GCAGCATCACTGAT	1 tttggtttctcacg	531 cgagaagaaattga 	471 ccaagcttgacagg             481 CCTATGTTGAACAG	11 ggatctaaaccaag 	0 aatgcgggagacac              ACATCTGGAAGCA	324 agtctcattatggatg:	4 gatcaattggaa              1 GATCAAGTACAA	204 gtcactgcttctaaa                 184 ACCACTGCATCTGAG	 124 TCTTCTGGGAAGGT
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itgattcatggtctcttcccagaggctgtcaccattggtgaagatgttagt 1610 	ttgaatgatat	1551 1561	рb
aatactttggatatgcaactgatgtagatgctgtggtttatttgatgctg 1550 	aactacaatga            AATTACAATGA	1491 1501	Qy Db
tgacttcaatgatgtacacccatcatggattgcaggtagattttaccggc 1490 	tttgatggggt             TTTGATGGTGT	1431 1441	Qy Db
tttcaaatgcaaggtggtggttggatgagtacaagtttgatgggttcaga 1430 	aggtttcttct            AGGTATCTTCT	1371 1381	Qy Db
attggatgtgggactctcgccttttcaactatgggagctgggaggttcta 1370 		1311 1321	Qy Db
ggctgaatatgtttgatggtacggatggtcactactttcactctggacca 1310 	acgttggatgg	1251 1261	Qy Db
	GCTCATGAGCT	1201	Дb

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STU011890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2571 tattgatcttcctatgttcatctgcgttgaacgaaatatattgagcctataattt 2625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2461 TATGCACCGTGCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2391 gatgcagagcacttcagctttgaagggtggtacgataccggcctcgatccttcatggtg 2450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2331 tacaagatagtcttggattcagatgatcctttgtttggaggctttggcaggcttagtcat 2390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaatgaa 2510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Direct Submission
Submitted (07-0CT-1998) Jobling S.A., Plant Science Unit, United (07-0CT-1998) Jobling S.A., Plant Science United (07-0CT-1998) Jobling S.A., Plant Science United (07-0CT-1998) Jobling Science (07-0CT-1998) Jobling Scien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potato.
Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 2992)
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DESDRIRERGIPPPGLGOKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
SRGYEKMGFTRSATGITYREWALGAGSSAALIGDENWNDANDLUTRNEEGVWEIFLPN
NVDGSPAIDHGSRVKIRMDTPSGVKDSIPAWINVSLQLPDEIPYNGIHYDPEEERFI
FQHPRPKKPKSLRIYESHIGMSSPEPKINSYVWFRDEVLPRIKKLGYNALQIMAIQIMA
SYYASFGYHVTNFFAPSSREGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="sequence SBE A-6"
140. .283
                                                                                                                                                                                                                                                               /LTABS181L10D="MYYTLSGYREPTYPSYYKSNGFSSNGDRRANVSYELKKHSLSR
KILLEKSSYNSEFRSSTYAAGGKYLYDGTGSDSSSSSTDGFETTETSDENSPASTDUD
SSTMEHASGIKTENDDVEPSSDLTGSVEELDFASSLGLQEGGKLEESKTLNTSEETII
                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
/product="starch branching enzyme II"
/protein_id="c,840/748.1"
/db_xref="GI:4584513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name="1,4-alpha-Glucan branching enzyme"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SBE II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum"
/cultivar="Desiree"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SBE II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on/Qualifiers
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BASE COUNT
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1067 tgttcagctcatggctattcaagagcattcatattatgctagttttgggtatcacgtcac 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                    1228 CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC 1287
                                                                                                                                                                                                                                   1168 AAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAA 1227
                                                                                                                                                                                                                                                                                                                                                                  1108 ACATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACCCCACGGCCAAAGAAACC 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1048 CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                827 tattcctgcttggatcaagttctcagttcaagcaccaggtgaactcccatataatggcat 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     988 AATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808 AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGC 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 aaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggagc 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748 ACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTTGGAAGCCTTTTCTCGTGGTTATGA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 agatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaag 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 TGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT1ATGAAAT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 TGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 tyttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcetcagaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688 AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG1 ACAAGAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                               cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc 1066
                                                                                                                                                                                                                                                                              aaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaa 1006
                                                                                                                                                                                                                                                                                                                                                                                                         atactatgatcctcccgaggaggaggtatgtgttcaaaaaatcctcagccaaagagacc 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aattccccatggttctcgagtaaagatacgcatggatactccatctggcaacaaagattc 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actoogagaagaaattgacaagtatgaaggtagtotggatgcattttcotogtggotatga 586
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284. .2785
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TSMMYLHHGLSYGFTGNYEEYFGLATTDVADAVVYLMLYNDLIFLGFDALTIGEDVSGM
PTFCIPVQEGGVGFDYRLHMAIADKRIELLKKRDEDWRVGDJYHTLTNRRWSEKCVSY
AESHDQALVGGNTIAFWLMDKOMYDFMALDRSGTSLIDRGIŁLKKMIRLYTMGLGGEG
YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRFRFDLGDAEYLRYRGLQ
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1598 tgaagatgttagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctt 1657
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                                                                                        1803 TTACATGATGTTAATGATCTCATTCACGGGCTCTTCCCTGAAGCTGTTTCAATTGG 1862
                                                                                                                                                                                                                        1743 ATCTTTTACCGGAAATTACAGTGAGTATTTTGGTTTAGCAACTGATGTTGAGGCTGTGGT 1802
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                                                                                                                               1538 ttatttgatgctgttgaatgatatgattcatggtctcttcccagaggctgtcaccattgg 1597
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RESULT AB029548

LOCUS DEFINITION

AB029548 Phaseolus AB029548

3360 bp mRNA PLN 1()-JUL-1999 algaris kbel mRNA for branching enzyme 1, complete

AB029548.1 GI:5441245

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

branching enzyme 1.
Phaseolus vulgaris cDNA to mRNA.
Phaseolus vulgaris cDNA to mRNA.
Enbaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;

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2763 TGAATCAGAGCCAATTGAACTGTCAGATGGAGTAGA 2798
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                                  2498 agtggagaatgaattggaacctgtcgccggttaaga 2533
                                                                         2703 ATCTTTCCTCGTTTATGCACCTTCTAGAACAGCAGTGGTGTATGCCCTTGCGGATGGAGT 2762
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                 acaccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaaatttgt 2053
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                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, F
State University. 103 Tyson Bldg., University Park, PA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Fisher, D.K., Gao, M., Kim, K.-N., Boyer, C.D. and Guiltinan, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2542)
Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guiltinan,M.J.
Two closely related cDNAs encoding starch branching enzyme from
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Query Match 47.8%; Score 1392.4; DB 14; Length 2542; Best Local Similarity 79.0%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 441; Indels 0;
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                                                                                                                                                                           1060 acaatgctgttcagctcatggctattcaagagcattcatattatgctagttttgggtatc 1119
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                                                          962 ATAATGCTGTTCAAATTATGGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACC 1021
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DQAMQHLEENYGFMTSBHQFISRKDEADRVIYFBRGDLVFNAUNVAIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H. Molecular cloning and characterization of starch-branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnoliophyta; eudicotyledons; core eudicots; ; Solanales; Solanaceae; Solanum.
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ASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEF
                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA03846.1"
/db_xref="GI:2764396"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="starch branching enzyme II, SBE-II"
                                                                                                                                                                                                                                                                                                                                    db_xref="SPTREMBL:049953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/cultivar-"Amanda"
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/function="branches 1,4-alpha glucans"
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                    1187 tanageteacgagttaggtettettgtteteatggatattgtteatageeatgcateaac
                                                                      1007
                                                                                                                  1127 aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga 1186
                                                                                                                                                                                                 1067 tgttcagctcatggctattcaagagcattcatattatgctagttttgggtatcacgtcac 1126
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                                                                                                                                                                                                                                                                       CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC
                                                                                                                                                                                                                                                                                                                                                                        AAAGT¢G¢tgagaatatatgaat¢tcatattggaatgagtagt¢cggag¢¢taaaattaa
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atactatgatcctcccgaggaggaggagtatgtgttcaaaaatcctcagccaaagagacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actccgagaagaaattgacaagtatgaaggtagtctggatgcattttctcgtggctatga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaagtttggtttctcacgcagtgaaacaggaattaacttatagagagtgggcaccaggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaag
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LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGD
AEYLAYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHW
TKSYSDYRIGCLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSRTAVVYALVDKEEEEEEEVAVVEEVVVEEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFDGFRFDGVTSIMYTHHGLSVGFTGNYKEYFGLATDVDAVVYLMLVNDLIHGLFPDA
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76.8%;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 512; Indels
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